

SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> New Hemolytic Proteins and Gene Coding Thereof

<130> SN-24_PCT

5 <150> JP10-88569

<151> 1998-04-01

<160> 5

<170> PatentIn Ver. 2.0

10 <210> 1

<211> 14

<212> PRT

<213> CARYBDEA RASTONII

15 <220>

<221> PEPTIDE

<222> (1)..(14)

<400> 1

20 Gly Glu Ile Gln Thr Lys Pro Asp Arg Val Gly Gln Ala Thr

1

5

10

<210> 2

<211> 18

25 <212> PRT

<213> CARYBDEA RASTONII

<220>

<221> PEPTIDE

<222> (1)..(18)

<400> 2

Gly Asn Ala Glu His Val Ala Ser Ala Val Glu Asn Ala Asn Arg Val

5 1 5 10 15

Asn Lys

<210> 3

<211> 15

10 <212> PRT

<213> CARYBDEA RASTONII

<400> 3

Met Ser Asp Gly Phe Tyr Thr Met Glu Asn Ser Asp Arg Arg Lys

15 1 5 10 15

<210> 4

<211> 1610

<212> DNA

20 <213> CARYBDEA RASTONII

<220>

<221> protein_bind

<222> (1)..(27)

25

<220>

<221> CDS

<222> (28)..(1380)

001021 "22544960

<220>

<221> protein_bind

<222> (1381)..(1610)

5 <400> 4

gcacaagcga ctgtgtgaag gaggacc atg att ctg aaa cat ctt cct tgg ctc 54

Met Ile Leu Lys His Leu Pro Trp Leu

1

5

ttt att gtc ctt gca att act tct gca aaa cat ggc aaa cgc tct gat 102

10 Phe Ile Val Leu Ala Ile Thr Ser Ala Lys His Gly Lys Arg Ser Asp

10 15 20 25

gtc aat tct tta ctt act aag gta gaa act gcc tta aaa gaa gct tct 150

Val Asn Ser Leu Leu Thr Lys Val Glu Thr Ala Leu Lys Glu Ala Ser

30

35

40

15 ggt agc aac gag gct gct ctt gag gct tta gag ggc tta aaa gga gag 198

Gly Ser Asn Glu Ala Ala Leu Glu Ala Leu Glu Gly Leu Lys Gly Glu

45

50

55

atc cag aca aaa cca gac cga gtt gga caa gcc aca aaa atc ctt gga 246

Ile Gln Thr Lys Pro Asp Arg Val Gly Gln Ala Thr Lys Ile Leu Gly

20 60 65 70

tct gtc gga tca gct cta gga aaa tta aat tct gga gat gca acc aaa 294

Ser Val Gly Ser Ala Leu Gly Lys Leu Asn Ser Gly Asp Ala Thr Lys

75

80

85

atc att tct ggt tgc ctc gac att gtt gca gga att gca aca act ttt 342

25 Ile Ile Ser Gly Cys Leu Asp Ile Val Ala Gly Ile Ala Thr Thr Phe

90 95 100 105

gga ggc cct gtc ggg atg gga atc gga gcc gta gct tct ttt gtt tct 390

Gly Gly Pro Val Gly Met Gly Ile Gly Ala Val Ala Ser Phe Val Ser

110

115

120

09647522-120100

tca att cta tca ttg ttt act gga agc tca gca aag aac tca gtt gct 438
 Ser Ile Leu Ser Leu Phe Thr Gly Ser Ser Ala Lys Asn Ser Val Ala
 125 130 135
 gcc gtt att gat aga gct tta agc aag cat cgc gat gag gcc atc caa 486
 5 Ala Val Ile Asp Arg Ala Leu Ser Lys His Arg Asp Glu Ala Ile Gln
 140 145 150
 aga cat gca gca ggt gcc aag aga gat ttt gct gaa tca tct gca ttc 534
 Arg His Ala Ala Gly Ala Lys Arg Asp Phe Ala Glu Ser Ser Ala Phe
 155 160 165
 10 att cag gtc atg aaa cag cag tcc aat ctt aca gat agc gac cta agt 582
 Ile Gln Val Met Lys Gln Gln Ser Asn Leu Thr Asp Ser Asp Leu Ser
 170 175 180 185
 atc att gca gcg aat gtt cct gtt tat aaa ttt agt aat ttt atc gga 630
 Ile Ile Ala Ala Asn Val Pro Val Tyr Lys Phe Ser Asn Phe Ile Gly
 15 190 195 200
 cag ttg gag agc aga att tcc caa ggc gca gca act acc agt ctt agc 678
 Gln Leu Glu Ser Arg Ile Ser Gln Gly Ala Ala Thr Thr Ser Leu Ser
 205 210 215
 gat gca aag aga gcc gtt gac ttc att ctg ctc tat tgt caa ctt gta 726
 20 Asp Ala Lys Arg Ala Val Asp Phe Ile Leu Leu Tyr Cys Gln Leu Val
 220 225 230
 gtc atg aga gaa acc ttg ctg gtc gac ttg gct att ctc tac agg aaa 774
 Val Met Arg Glu Thr Leu Leu Val Asp Leu Ala Ile Leu Tyr Arg Lys
 235 240 245
 25 gga aat gca gaa cac gtg gca agt gct gtg gaa aac gct aat agg gta 822
 Gly Asn Ala Glu His Val Ala Ser Ala Val Glu Asn Ala Asn Arg Val
 250 255 260 265
 aac aaa gag cta gct gct gat acc cta gat ttt ctt cat aaa ttg att 870
 Asn Lys Glu Leu Ala Ala Asp Thr Leu Asp Phe Leu His Lys Leu Ile

	270	275	280	
	cct gaa caa gca ttg ata ggt gca gtt tat cat cca att tct gcc tct			918
	Pro Glu Gln Ala Leu Ile Gly Ala Val Tyr His Pro Ile Ser Ala Ser			
	285	290	295	
5	gaa act agc aaa gca ata tta aat tac acg aaa tac ttt gga gtt cca			966
	Glu Thr Ser Lys Ala Ile Leu Asn Tyr Thr Lys Tyr Phe Gly Val Pro			
	300	305	310	
	gat gtt ccc cgt cct att gga aac cgc aga tac aaa ttt aca aat agt			1014
	Asp Val Pro Arg Pro Ile Gly Asn Arg Arg Tyr Lys Phe Thr Asn Ser			
10	315	320	325	
	tac tgg aat acc tac agt ata tgc agt gag gct tac atg gga aat tac			1062
	Tyr Trp Asn Thr Tyr Ser Ile Cys Ser Glu Ala Tyr Met Gly Asn Tyr			
	330	335	340	345
	atg ttc aga ggc tgt tct aac gtt cgg aat cca aat atc agg gta tcc			1110
15	Met Phe Arg Gly Cys Ser Asn Val Arg Asn Pro Asn Ile Arg Val Ser			
	350	355	360	
	aaa atg tct gat ggg ttt tac acc atg gag aat agc gat cgg agg aag			1158
	Lys Met Ser Asp Gly Phe Tyr Thr Met Glu Asn Ser Asp Arg Arg Lys			
	365	370	375	
20	ttg tat atc acc aag cat gac caa gga tgg gga tgg ggt act ttg gat			1206
	Leu Tyr Ile Thr Lys His Asp Gln Gly Trp Gly Trp Gly Thr Leu Asp			
	380	385	390	
	gag gat cca ggt gac caa ggc cat atg agg ttc att cct ttg aga cat			1254
	Glu Asp Pro Gly Asp Gln Gly His Met Arg Phe Ile Pro Leu Arg His			
25	395	400	405	
	ggg aag tat atg gta agc tct aag agg tgg ccc aac tgg ttc atg tat			1302
	Gly Lys Tyr Met Val Ser Ser Lys Arg Trp Pro Asn Trp Phe Met Tyr			
	410	415	420	425
	atg gaa tca agt gcc agt ggc tac att cgc agc tgg gaa aat aat cca			1350

Met Glu Ser Ser Ala Ser Gly Tyr Ile Arg Ser Trp Glu Asn Asn Pro

430

435

440

gga cct caa gga cat tgg agt ata aca taa ttaaagagga atcaacaatg 1400

Gly Pro Gln Gly His Trp Ser Ile Thr

5

445

450

tcccaaaggc atacgaatat aagacatcaa acgaatgcag tacttaaagt gcacacttgt 1460

atttctacat aggatgtcgt catgaaagtc cataaaccat ccagcggact aatttcatat 1520

taaacattaa tgtttcctta taatgcattt tcatgaaatc tctattgtga catttcaaga 1580

ggatatgttt gaaagaaaca aaaaaaaaaa 1610

10

<210> 5

<211> 450

<212> PRT

<213> CARYBDEA RASTONII

15

<400> 5

Met Ile Leu Lys His Leu Pro Trp Leu Phe Ile Val Leu Ala Ile Thr

1

5

10

15

Ser Ala Lys His Gly Lys Arg Ser Asp Val Asn Ser Leu Leu Thr Lys

20

20

25

30

Val Glu Thr Ala Leu Lys Glu Ala Ser Gly Ser Asn Glu Ala Ala Leu

35

40

45

Glu Ala Leu Glu Gly Leu Lys Gly Glu Ile Gln Thr Lys Pro Asp Arg

50

55

60

25

Val Gly Gln Ala Thr Lys Ile Leu Gly Ser Val Gly Ser Ala Leu Gly

65

70

75

80

Lys Leu Asn Ser Gly Asp Ala Thr Lys Ile Ile Ser Gly Cys Leu Asp

85

90

95

Ile Val Ala Gly Ile Ala Thr Thr Phe Gly Gly Pro Val Gly Met Gly

00T02T 2254960

	100	105	110	
	Ile Gly Ala Val Ala Ser Phe Val Ser Ser Ile Leu Ser Leu Phe Thr			
	115	120	125	
	Gly Ser Ser Ala Lys Asn Ser Val Ala Ala Val Ile Asp Arg Ala Leu			
5	130	135	140	
	Ser Lys His Arg Asp Glu Ala Ile Gln Arg His Ala Ala Gly Ala Lys			
	145	150	155	160
	Arg Asp Phe Ala Glu Ser Ser Ala Phe Ile Gln Val Met Lys Gln Gln			
	165	170	175	
10	Ser Asn Leu Thr Asp Ser Asp Leu Ser Ile Ile Ala Ala Asn Val Pro			
	180	185	190	
	Val Tyr Lys Phe Ser Asn Phe Ile Gly Gln Leu Glu Ser Arg Ile Ser			
	195	200	205	
	Gln Gly Ala Ala Thr Thr Ser Leu Ser Asp Ala Lys Arg Ala Val Asp			
15	210	215	220	
	Phe Ile Leu Leu Tyr Cys Gln Leu Val Val Met Arg Glu Thr Leu Leu			
	225	230	235	240
	Val Asp Leu Ala Ile Leu Tyr Arg Lys Gly Asn Ala Glu His Val Ala			
	245	250	255	
20	Ser Ala Val Glu Asn Ala Asn Arg Val Asn Lys Glu Leu Ala Ala Asp			
	260	265	270	
	Thr Leu Asp Phe Leu His Lys Leu Ile Pro Glu Gln Ala Leu Ile Gly			
	275	280	285	
	Ala Val Tyr His Pro Ile Ser Ala Ser Glu Thr Ser Lys Ala Ile Leu			
25	290	295	300	
	Asn Tyr Thr Lys Tyr Phe Gly Val Pro Asp Val Pro Arg Pro Ile Gly			
	305	310	315	320
	Asn Arg Arg Tyr Lys Phe Thr Asn Ser Tyr Trp Asn Thr Tyr Ser Ile			
	325	330	335	

Cys Ser Glu Ala Tyr Met Gly Asn Tyr Met Phe Arg Gly Cys Ser Asn

340

345

350

Val Arg Asn Pro Asn Ile Arg Val Ser Lys Met Ser Asp Gly Phe Tyr

355

360

365

5 Thr Met Glu Asn Ser Asp Arg Arg Lys Leu Tyr Ile Thr Lys His Asp

370

375

380

Gln Gly Trp Gly Trp Gly Thr Leu Asp Glu Asp Pro Gly Asp Gln Gly

385

390

395

400

His Met Arg Phe Ile Pro Leu Arg His Gly Lys Tyr Met Val Ser Ser

10

405

410

415

Lys Arg Trp Pro Asn Trp Phe Met Tyr Met Glu Ser Ser Ala Ser Gly

420

425

430

Tyr Ile Arg Ser Trp Glu Asn Asn Pro Gly Pro Gln Gly His Trp Ser

435

440

445

15

Ile Thr

450

20

001021" 22544960